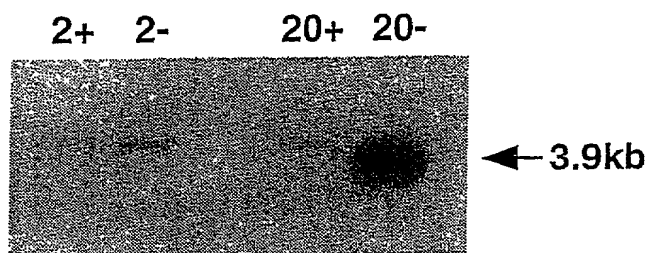


HP95	1	-----MIVADSEC-R-----AELK-----DYLRF-----PG-CVGDS-----
PA26	1	MAEGENEVRWDGLCSRDSTTRETALENIROITILRKTEYLRSVKETPHRPSDGSNTESSD
HP95	27	G-----PGEHORES-----RAR--RGPR-----GPSAFIPVEFVLREG
PA26	61	GLNKLLAHLMLSKRCPEKDVREKSEFILKSIQELGIRIPRPLGCGPSRFIEKEFLQVG
HP95	58	AESLEQH-LGLAALMSSGRVDNAVMGLHPDYFTSFXXLHYLLHTDGPJASSMRHYIA
PA26	121	SEDAQMHALFADSFAALGRIDNTVMVFHPOYLESEFKTQHYLLQMDGPLPLHYRHYIG
HP95	117	IMAAARHQCXYLVGSHMAEFLQTGGDPEWILGLHRAPEKIRKLTSEINKLAHRPWLITKE
PA26	181	IMAAARHQCXYLVNLHVNDELHVGGDPKWINGLENAPOKIQNLGEINKLAHRPWLITKE
HP95	177	HTQALLKTGEHWSLAELQALVLLTHCHSLSSVFEGCGILPEGDADGSPAPQAPPPS-
PA26	241	HTEGLLKAEHWSLAELHAAVLLTHYHSLASFTFGCGISPEIHCDGGHTFRPPPSVSNY
HP95	236	---TQSSP-PSRD--PLN---NSGFFESARDVEALMERMQLOESLLRDEG-TSQEEMES
PA26	301	CICDIINGNHSVDEMPANSAENVSVSDSFFVEALMEKMRQLOE--CRDEEEASQEEMAS
HP95	286	REFEKSESLVTPSADILEPSPHPDYLCFVEDPTGYEDFRRGAQAPPTFRAQDYTWE
PA26	359	REFEKRESMFVFSDD-EEVTPARAVSRHEDTSYGYKDFSRGMHVP-TERVQDYQWE
HP95	346	DHGYSLLIORLYPFGGQLDEKFOAAYSLTYNTAMHSGVDTSVLRRAIWNYYTHCFGIRY
PA26	417	DHGYSLLIORLYPFGVQLDEKFIAYNLTYNTAMHKVDVTSVLRRAIWNYYTHCFGIRY
HP95	406	DDYDYGEVNOQLLERNLKVYIKTVACYPEKTTVMYNLFWRHFRHSEKVVHVNLLL EARMQ
PA26	477	DDYDYGEVNOQLLRSFKVYIKTVCTPEKVTVMYDSFWRQFHSEKVVHVNLLL EARMQ
HP95	466	AALLALRAITRYMT
PA26	537	AALLALRAITRYMT

FIGURE 1

A



B

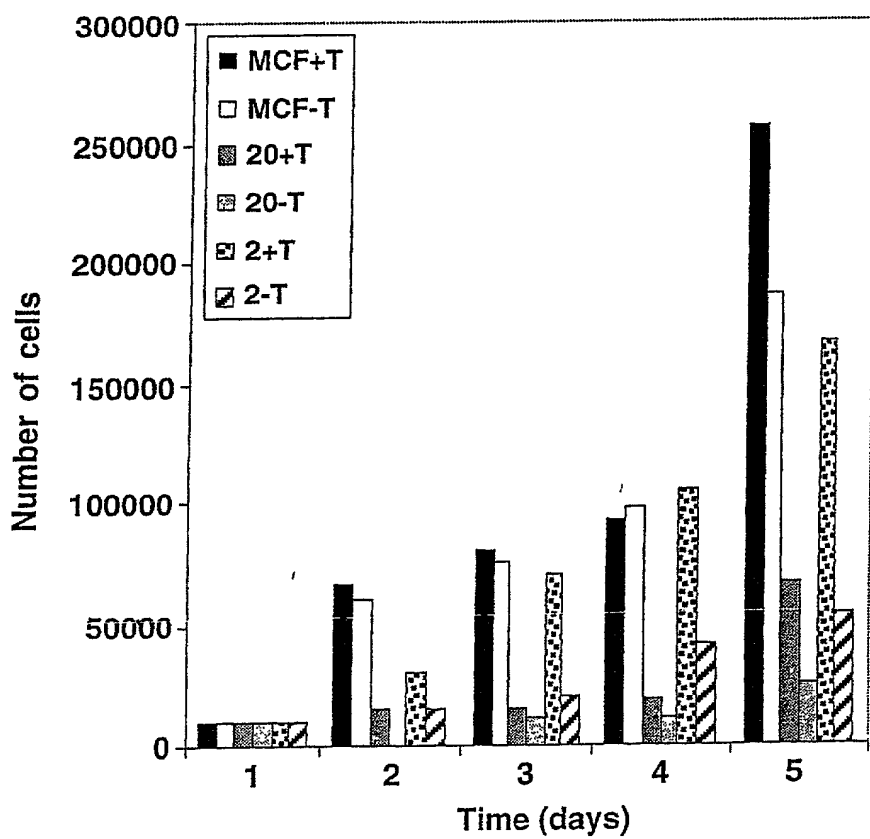


FIGURE 2

FIG. 3

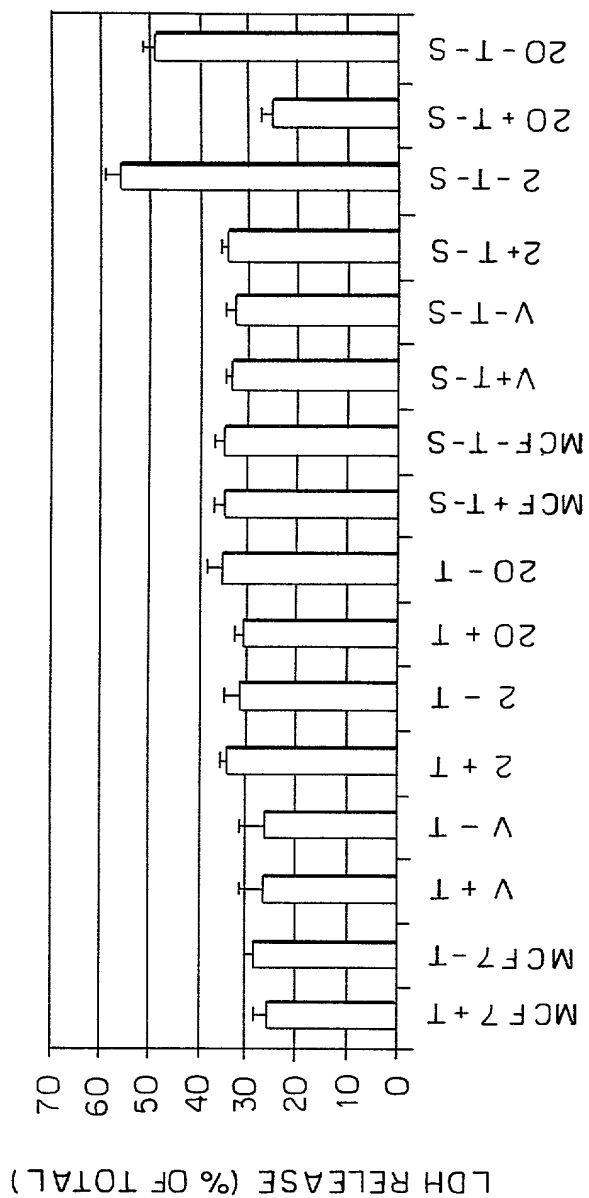
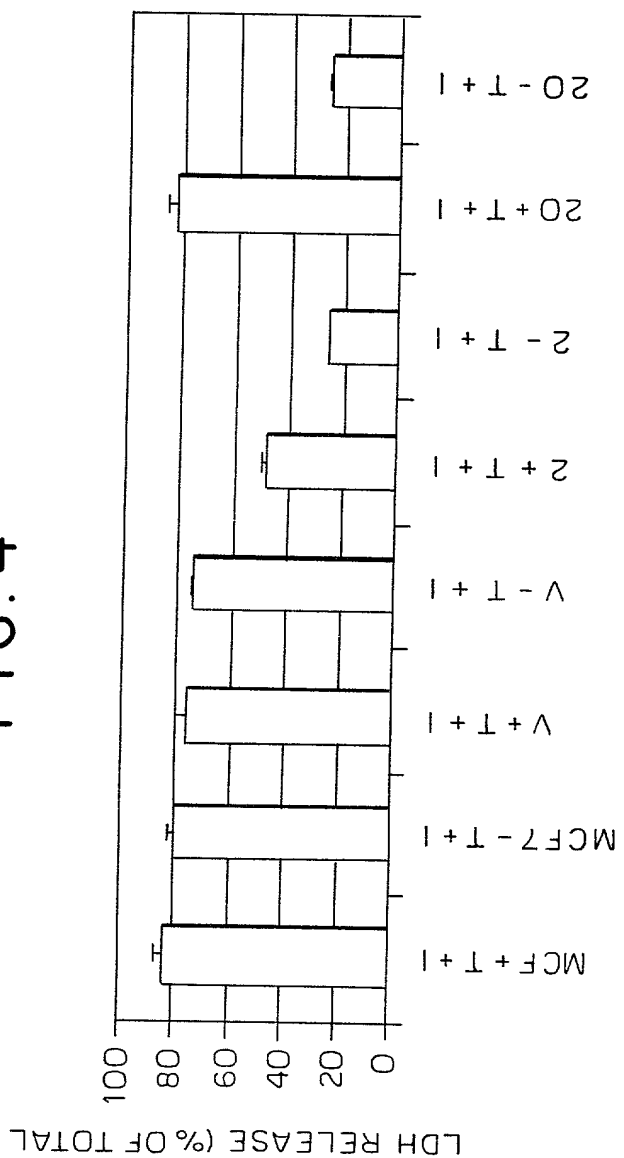


FIG. 4



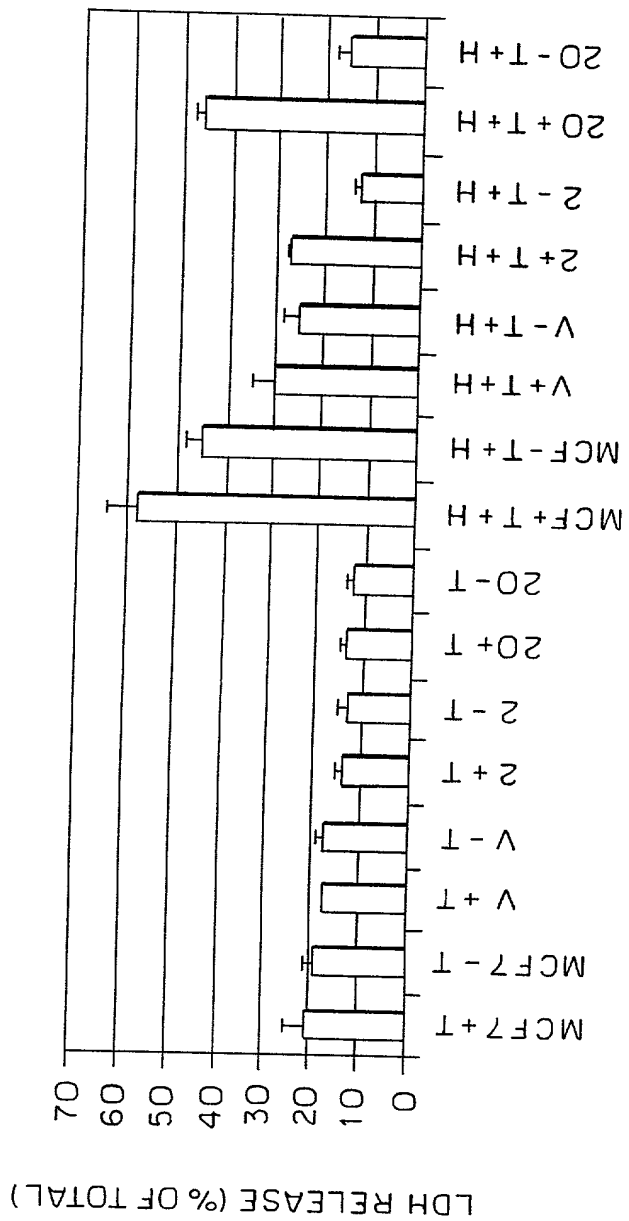


FIG. 5